

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Fisher, Douglas A.
 Gooding, Douglas H.
 Streeter, David Gray

(ii) TITLE OF THE INVENTION: CYCLIC-GMP PHOSPHODIESTERASE

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 (B) STREET: 3174 Porter Dr.
 (C) CITY: Palo Alto
 (D) STATE: CA
 (E) COUNTRY: USA
 (F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
 (B) COMPUTER: IBM Compatible
 (C) OPERATING SYSTEM: DOS
 (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned
 (B) FILING DATE: Filed Herewith
 (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
 (B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.
 (B) REGISTRATION NUMBER: 36,749
 (C) REFERENCE/DOCKET NUMBER: PF-0442 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555
 (B) TELEFAX: 650-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 593 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: PROSNOT06
 (B) CLONE: 828228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Gly	Ser	Gly	Ser	Ser	Ser	Tyr	Arg	Pro	Lys	Ala	Ile	Tyr	Leu	Asp
1															
														15	
Ile	Asp	Gly	Arg	Ile	Gln	Lys	Val	Ile	Phe	Ser	Lys	Tyr	Cys	Asn	Ser
														20	
														25	
															30
Ser	Asp	Ile	Met	Asp	Leu	Phe	Cys	Ile	Ala	Thr	Gly	Leu	Pro	Arg	Asn

35	40	45
Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp		
50	55	60
Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro		
65	70	75
Val Ala Ile Lys Gln Leu Ser Ala Gly Val Glu Asp Lys Arg Thr Thr		
85	90	95
Ser Arg Gly Gln Ser Ala Glu Arg Pro Leu Arg Asp Arg Arg Val Val		
100	105	110
Gly Leu Glu Gln Pro Arg Arg Glu Gly Ala Phe Glu Ser Gly Gln Val		
115	120	125
Glu Pro Arg Pro Arg Glu Pro Gln Gly Cys Tyr Gln Glu Gly Gln Arg		
130	135	140
Ile Pro Pro Glu Arg Glu Glu Leu Ile Gln Ser Val Leu Ala Gln Val		
145	150	155
Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu Lys Ala Glu		
165	170	175
Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu Leu Glu Gly		
180	185	190
Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile Lys Lys Met		
195	200	205
Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys Pro Cys Lys		
210	215	220
Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg Arg Asp Val		
225	230	235
Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile Glu Ala Leu		
245	250	255
Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn Glu Met Leu		
260	265	270
Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val Arg Asp Phe		
275	280	285
Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys Val His Asp		
290	295	300
Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val		
305	310	315
Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys		
325	330	335
Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His		
340	345	350
Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg		
355	360	365
Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His		
370	375	380
His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile		
385	390	395
Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met		
405	410	415
Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met		
420	425	430
Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu		
435	440	445
His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser		
450	455	460
Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu		
465	470	475
Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu		
485	490	495
Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala		
500	505	510
Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val		
515	520	525
Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp		
530	535	540
Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met		
545	550	555
		560

Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu
 565 570 575
 Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Gly Asp Cys
 580 585 590
 Ala

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1997 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNOT06
- (B) CLONE: 828228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCTCCCCGCG	GCGGCTGGCG	TGGGAAAGT	ACAGTAAAAA	GTCCGAGTGC	AGCCGCCGG	60
CGCAGGATGG	GATCCGGCTC	CTCCAGCTAC	CGGCCCAAGG	CCATCTACCT	GGACATCGAT	120
GGACGCATT	AGAAGGTAAT	CTTCAGCAAG	TACTGCAACT	CCAGCGACAT	CATGGACCTG	180
TTCTGCATCG	CCACCGGCC	GCCTCGGAAC	ACGACCATCT	CCCTGCTGAC	CACCGACGAC	240
GCCATGGTCT	CCATCGACCC	CACCATGCC	GCGAATTTCAG	AACGCACCTC	GTACAAAGTG	300
AGACCTGTGG	CCATCAAGCA	ACTCTCCGCT	GGTGTGAGG	ACAAGAGAAC	CACAAGCCGT	360
GGCCAGTC	CTGAGAGAAC	ACTGAGGGAC	AGACGGGTTG	TGGCCCTGGA	GCAGCCCCGG	420
AGGGAAGGAG	CATTGAAAG	TGGACAGGTA	GAGCCCAGGC	CCAGAGAGGC	CCAGGGCTGC	480
TACCAAGGAG	GCCAGCGCAT	CCCTCCAGAG	AGAGAAGAAT	TAATCCAGAG	CGTGCTGGCG	540
CAGGTTGAG	AGCAGTTCTC	AAGAGCATTC	AAAATCAATG	AACTGAAAGC	TGAAGTTGCA	600
AATCACTTGG	CTGTCCCTAGA	AAAACCGGTG	GAATTGAAAG	GACTAAAAAGT	GGTGGAGATT	660
GAGAAATGCA	AGAGTGACAT	TAAGAAGATG	AGGGAGGAGC	TGGCGGCCAG	AAGCAGCAGG	720
ACCAACTGCC	CCTGTAAGTA	CAGTTTTTG	GATAACCACA	AGAAGTTGAC	TCCTCGACGC	780
GATGTTCCCA	CTTACCCCAA	GTACCTGCTC	TCTCCAGAGA	CCATCGAGGC	CCTGCGGAAG	840
CCGACCTTTG	ACGTCTGGCT	TTGGGAGCCC	AATGAGATGC	TGAGCTGCCT	GGAGCACATG	900
TACCAAGGACC	TCGGGCTGGT	CAGGGACTTC	AGCATCAACC	CTGTCACCCCT	CAGGAGGTGG	960
CTGTTCTGTG	TCCACGACAA	CTACAGAAAC	AACCCCTTCC	ACAACCTCCG	GCACTGCTTC	1020
TGCGTGGCCC	AGATGATGTA	CAGCATGGTC	TGGCTCTGCA	GTCTCCAGGA	GAAGTTCTCA	1080
CAAACGGATA	TCCTGATCCT	AATGACAGCG	GCCATCTGCC	ACGATCTGGA	CCATCCCAGC	1140
TACAACAACA	CGTACCAAGAT	CAATGCCCGC	ACAGAGCTGG	CGGTCCGCTA	CAATGACATC	1200
TCACCGCTGG	AGAACCCACCA	CTGCGCCGTG	GCCTTCCAGA	TCCTCGCCGA	GCCTGAGTGC	1260
AAACATCTCT	CCAACATCCC	ACCTGATGGG	TTCAAGCAGA	TCCGACAGGG	AATGATCACA	1320
TTAATCTTGG	CCACTGACAT	GGCAAGACAT	GCAGAAATT	TGGATTCTTT	CAAAGAGAAA	1380
ATGAGAATT	TTGACTACAG	CAACGAGGAG	CACATGCC	TGCTGAAGAT	GATTTTGATA	1440
AAATGCTGTG	ATATCTCTAA	CGAGGTCCGT	CCAATGGAAG	TCGCGAGAGC	TTGGGTGGAC	1500
TGTTTATTAG	AGGAATATTT	TATGCAGAGC	GACCGTGAGA	AGTCAGAAGG	CCTTCCTGTG	1560
GCACCGTTCA	TGGACCGAGA	CAAAGTGACC	AAGGCCACAG	CCCAGATTGG	GTTCATCAAG	1620
TTTGTCTCTGA	TCCCAATGTT	TGAAACAGTG	ACCAAGCTCT	TCCCCATGGT	TGAGGAGATC	1680
ATGCTGCAGC	CACTTGGGA	ATCCCGAGAT	CGCTACCGAGG	AGCTGAAGCG	GATAGATGAC	1740
GCCATGAAAG	AGTTACAGAA	GAAGACTGAC	AGCTTGACGT	CTGGGGCCAC	CGAGAAGTCC	1800
AGAGAGAGAA	GCAGAGATGT	AAAAAACAGT	GAAGGAGACT	GTGCCGTGAGG	AAAGCGGGGG	1860
GCGTGGCTGC	AGTTCTGGAC	GGGCTGGCCG	AGCTGCCGG	GATCCTTGTG	CAGGAAAGAG	1920
CTGCCCTGGG	CACCTGGCAC	CACAAGACCA	TGTTTCTAA	GAACCATT	GTTCACTGAT	1980
ACAAAAAA	AAAAAAA					1997

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 713 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THP1PLB02

(B) CLONE: 156196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Leu Ala Cys Phe Leu Asp Lys His His Asp Ile Ile Ile Asp His
 1 5 10 15
 Arg Asn Pro Arg Gln Leu Asp Ala Glu Ala Leu Cys Arg Ser Ile Arg
 20 25 30
 Ser Ser Lys Leu Ser Glu Asn Thr Val Ile Val Gly Val Val Arg Arg
 35 40 45
 Val Asp Arg Glu Glu Leu Ser Val Met Pro Phe Ile Ser Ala Gly Phe
 50 55 60
 Thr Arg Arg Tyr Val Glu Asn Pro Asn Ile Met Ala Cys Tyr Asn Glu
 65 70 75 80
 Leu Leu Gln Leu Glu Phe Gly Glu Val Arg Ser Gln Leu Lys Leu Arg
 85 90 95
 Ala Cys Asn Ser Val Phe Thr Ala Leu Glu Asn Ser Glu Asp Ala Ile
 100 105 110
 Glu Ile Thr Ser Glu Asp Arg Phe Ile Gln Tyr Ala Asn Pro Ala Phe
 115 120 125
 Glu Thr Thr Met Gly Tyr Gln Ser Gly Glu Leu Ile Gly Lys Glu Leu
 130 135 140
 Gly Glu Val Pro Ile Asn Glu Lys Lys Ala Asp Leu Leu Asp Thr Ile
 145 150 155 160
 Asn Ser Cys Ile Arg Ile Gly Lys Glu Trp Gln Gly Ile Tyr Tyr Ala
 165 170 175
 Lys Lys Lys Asn Gly Asp Asn Ile Gln Gln Asn Val Lys Ile Ile Pro
 180 185 190
 Val Ile Gly Gln Gly Lys Ile Arg His Tyr Val Ser Ile Ile Arg
 195 200 205
 Val Cys Asn Gly Asn Asn Lys Ala Glu Lys Ile Ser Glu Cys Val Gln
 210 215 220
 Ser Asp Thr Arg Thr Asp Asn Gln Thr Gly Lys His Lys Asp Arg Arg
 225 230 235 240
 Lys Gly Ser Leu Asp Val Lys Ala Val Ala Ser Arg Ala Thr Glu Val
 245 250 255
 Ser Ser Gln Arg Arg His Ser Ser Met Ala Arg Ile His Ser Met Thr
 260 265 270
 Ile Glu Ala Pro Ile Thr Lys Val Ile Asn Val Ile Asn Ala Ala Gln
 275 280 285
 Glu Ser Ser Pro Met Pro Val Thr Glu Ala Leu Asp Arg Val Leu Glu
 290 295 300
 Ile Leu Arg Thr Thr Glu Leu Tyr Ser Pro Gln Phe Gly Ala Lys Asp
 305 310 315 320
 Asp Asp Pro His Ala Asn Asp Leu Val Gly Gly Leu Met Ser Asp Gly
 325 330 335
 Leu Arg Arg Leu Ser Gly Asn Glu Tyr Val Leu Ser Thr Lys Asn Thr
 340 345 350
 Gln Met Val Ser Ser Asn Ile Ile Thr Pro Ile Ser Leu Asp Asp Val
 355 360 365
 Pro Pro Arg Ile Ala Arg Ala Met Glu Asn Glu Glu Tyr Trp Asp Phe
 370 375 380
 Asp Ile Phe Glu Leu Glu Ala Ala Thr His Asn Arg Pro Leu Ile Tyr
 385 390 395 400
 Leu Gly Leu Lys Met Phe Ala Arg Phe Gly Ile Cys Glu Phe Leu His
 405 410 415
 Cys Ser Glu Ser Thr Leu Arg Ser Trp Leu Gln Ile Ile Glu Ala Asn
 420 425 430
 Tyr His Ser Ser Asn Pro Tyr His Asn Ser Thr His Ser Ala Asp Val
 435 440 445
 Leu His Ala Thr Ala Tyr Phe Leu Ser Lys Glu Arg Ile Lys Glu Thr
 450 455 460
 Leu Asp Pro Ile Asp Glu Val Ala Ala Leu Ile Ala Ala Thr Ile His
 465 470 475 480
 Asp Val Asp His Pro Gly Arg Thr Asn Ser Phe Leu Cys Asn Ala Gly
 485 490 495

Ser Glu Leu Ala Ile Leu Tyr Asn Asp Thr Ala Val Leu Glu Ser His
 500 505 510
 His Ala Ala Leu Ala Phe Gln Leu Thr Thr Gly Asp Asp Lys Cys Asn
 515 520 525
 Ile Phe Lys Asn Met Glu Arg Asn Asp Tyr Arg Thr Leu Arg Gln Gly
 530 535 540
 Ile Ile Asp Met Val Leu Ala Thr Glu Met Thr Lys His Phe Glu His
 545 550 555 560
 Val Asn Lys Phe Val Asn Ser Ile Asn Lys Pro Leu Ala Thr Leu Glu
 565 570 575
 Glu Asn Gly Glu Thr Asp Lys Asn Gln Glu Val Ile Asn Thr Met Leu
 580 585 590
 Arg Thr Pro Glu Asn Arg Thr Leu Ile Lys Arg Met Leu Ile Lys Cys
 595 600 605
 Ala Asp Val Ser Asn Pro Cys Arg Pro Leu Gln Tyr Cys Ile Glu Trp
 610 615 620
 Ala Ala Arg Ile Ser Glu Glu Tyr Phe Ser Gln Thr Asp Glu Glu Lys
 625 630 635 640
 Gln Gln Gly Leu Pro Val Val Met Pro Val Phe Asp Arg Asn Thr Cys
 645 650 655
 Ser Ile Pro Lys Ser Gln Ile Ser Phe Ile Asp Tyr Phe Ile Thr Asp
 660 665 670
 Met Phe Asp Ala Trp Asp Ala Phe Val Asp Leu Pro Asp Leu Met Gln
 675 680 685
 His Leu Asp Asn Asn Phe Lys Tyr Trp Lys Gly Leu Asp Glu Met Lys
 690 695 700
 Leu Arg Asn Leu Arg Pro Pro Pro Glu
 705 710

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 829179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Phe Gln His Gln Thr Asn Pro Gly Gly Pro Thr Asn Arg Arg Arg
 1 5 10 15
 Pro Arg Asp Gln Glu Ile His Gln Glu Pro Arg Tyr Pro Lys Ala Arg
 20 25 30
 Arg His Thr Pro Ala Trp Pro Pro Thr Gln Ser Arg Ser Trp Thr Gly
 35 40 45
 Ala Ser Thr Ser Trp Arg Pro Ser Arg Pro Ile Ala Ala Ser Pro Thr
 50 55 60
 Trp Arg Arg Leu Ser Ser Asn Ala Cys Ser Thr Arg Ser Cys Arg Thr
 65 70 75 80
 Leu Ala Ser Pro Ala Asp Arg Glu Ile Arg Phe Pro Asn Ile Tyr Val
 85 90 95
 Pro His Phe Trp Asp Lys Gln Gln Glu Phe Asp Leu Pro Ser Leu Arg
 100 105 110
 Val Glu Asp Asn Pro Glu Leu Val Ala Ala Asn Ala Ala Gly Gln
 115 120 125
 Gln Ser Ala Gly Gln Tyr Ala Arg Ser Arg Ser Pro Arg Gly Pro Pro
 130 135 140
 Met Ser Gln Ile Ser Gly Val Lys Arg Pro Leu Ser His Thr Asn Ser
 145 150 155 160
 Phe Thr Gly Glu Arg Leu Pro Thr Phe Gly Val Glu Thr Pro Arg Glu
 165 170 175
 Asn Glu Leu Gly Thr Leu Leu Gly Glu Leu Asp Thr Trp Gly Ile Gln

180	185	190
Ile Phe Ser Ile Gly Glu Phe Ser Val Asn Arg Pro Leu Thr Cys Val		
195	200	205
Ala Tyr Thr Ile Phe Gln Ser Arg Glu Leu Leu Thr Ser Leu Met Ile		
210	215	220
Pro Pro Lys Thr Phe Leu Asn Phe Met Ser Thr Leu Glu Asp His Tyr		
225	230	235
Val Lys Asp Asn Pro Phe His Asn Ser Leu His Ala Ala Asp Val Thr		
245	250	255
Gln Ser Thr Asn Val Leu Leu Asn Thr Pro Ala Leu Glu Gly Val Phe		
260	265	270
Thr Pro Leu Glu Val Gly Gly Ala Leu Phe Ala Ala Cys Ile His Asp		
275	280	285
Val Asp His Pro Gly Leu Thr Asn Gln Phe Leu Val Asn Ser Ser Ser		
290	295	300
Glu Leu Ala Leu Met Tyr Asn Asp Glu Ser Val Leu Glu Asn His His		
305	310	315
Leu Ala Val Ala Phe Lys Leu Leu Gln Asn Gln Gly Cys Asp Ile Phe		
325	330	335
Cys Asn Met Gln Lys Lys Gln Arg Gln Thr Leu Arg Lys Met Val Ile		
340	345	350
Asp Ile Val Leu Ser Thr Asp Met Ser Lys His Met Ser Leu Leu Ala		
355	360	365
Asp Leu Lys Thr Met Val Glu Thr Lys Lys Val Ala Gly Ser Gly Val		
370	375	380
Leu Leu Leu Asp Asn Tyr Thr Asp Arg Ile Gln Val Leu Glu Asn Leu		
385	390	395
Val His Cys Ala Asp Leu Ser Asn Pro Thr Lys Pro Leu Pro Leu Tyr		
405	410	415
Lys Arg Trp Val Ala Leu Leu Met Glu Glu Phe Phe Leu Gln Gly Asp		
420	425	430
Lys Glu Arg Glu Ser Gly Met Asp Ile Ser Pro Met Cys Asp Arg His		
435	440	445
Asn Ala Thr Ile Glu Lys Ser Gln Val Gly Phe Ile Asp Tyr Ile Val		
450	455	460
His Pro Leu Trp Glu Thr Trp Ala Ser Leu Val His Pro Asp Ala Gln		
465	470	475
Asp Ile Leu Asp Thr Leu Glu Glu Asn Arg Asp Tyr Tyr Gln Ser Met		
485	490	495
Ile Pro Pro Ser Pro Pro Ser Gly Val Asp Glu Asn Pro Gln Glu		
500	505	510
Asp Arg Ile Arg Phe Gln Val Thr Leu Glu Glu Ser Asp Gln Glu Asn		
515	520	525
Leu Ala Glu Leu Glu Glu Gly Asp Glu Ser Gly Gly Glu Thr Thr Thr		
530	535	540
Thr Gly Thr Thr Gly Thr Ala Ala Ser Ala Leu Arg Ala Gly Gly		
545	550	555
Gly Gly Gly Gly Gly Gly Met Ala Pro Arg Thr Gly Gly Cys Gln		
565	570	575
Asn Gln Pro Gln His Gly Gly Met		
580		

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGGTGACAGG GTTGATGCT

19

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TCGCTTAGTT TTACCGTTTT C

21

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TATCGCCTCC ATCAACAAAC TT

22

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GACACAGAAC AGCCACCTC

19

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AGCAAGTTCA GCCTGGTTAA G

21

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTTATGAGTA TTTCTTCAG GGTA

24

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATCATGGTTA CAAATTATCG AAGCCAATTA

30

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCTCCTCCCT CATCTTCTTA

20

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGGACAGCCA AGTGATT

18

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGCGCTGGCC TTCCTGGTAG

20